

# SEQUENCE LISTING

<110> Wang, Yan  
 Xi, Lei  
 Prosen, Dennis E.  
 MJ Bioworks, Inc.

<120> Improved Nucleic Acid Modifying Enzymes

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<140> US 09/870,353

<141> 2001-05-30

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<151> 2000-05-26

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gactatagac aaaaagcgat aaaactctta gcaaattctt tctacggata ttatggctat 1500
gcaaaagcaa gatggtactg taaggagtgt gctgagagcg ttactgcctg gggaagaaaag 1560
tacatcgagt tagtatggaa ggagctcgaa gaaaagtgtg gatttaaagt cctctacatt 1620
gacatcgatg gtctctatgc aactatccca ggaggagaaa gtgaggaaat aaagaaaaag 1680
gctctagaat ttgtaaaata cataaattca aagctccctg gactgctaga gcttgaatat 1740
gaagggtttt ataagagggg attcttcggt acgaagaaga ggtatgcagt aatagatgaa 1800
gaaggaaaag tcattactcg tggtttagag atagttagga gagattggag tgaaattgca 1860
aaagaaactc aagctagagt tttggagaca atactaaaac acggagatgt tgaagaagct 1920
gtgagaatag taaaagaagt aatacaaaaag cttgccatt atgaaattcc accagagaag 1980
ctcgcaatat atgagcagat aacaagacca ttacatgagt ataaggcgat aggtcctcac 2040
gtagctgttg caaagaaact agctgctaaa ggagttaaaa taaagccagg aatggtaatt 2100
ggatacatag tacttagagg cgatgggtcca attagcaata gggcaattct agctgaggaa 2160
tacgatccca aaaagcacia gtatgacgca gaatattaca ttgagaacca ggttcttcca 2220
gcggtactta ggatattgga gggatttgga tacagaaaag aagacctcag atacaaaaag 2280
acaagacaag tcggcctaac ttcttggtt aacattaaaa aatccggtac cggcgggtggc 2340
ggtgcaaccg taaagttcaa gtacaaaggc gaagaaaaag aggtagacat ctccaagatc 2400
aagaaagtat ggcgtgtggg caagatgatc tccttcacct acgacgaggg cggtggaag 2460
accggccgtg gtgcggtgta cgaaaaggac gcgccgaagg agctgctgca gatgctggag 2520
aagcagaaaa agtga 2535

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<210> 8
<211> 844
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:fusion protein
      Pfu-Ssod7d

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<400> 8
Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
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Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg
      20             25             30
Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
      35             40             45
Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
      50             55             60
Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
      65             70             75             80
Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
      85             90             95
Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
      100            105            110
Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
      115            120            125

```



Met	Glu	Gly	Glu	Glu	Glu	Leu	Lys	Ile	Leu	Ala	Phe	Asp	Ile	Glu	Thr	130	135	140
Leu	Tyr	His	Glu	Gly	Glu	Glu	Phe	Gly	Lys	Gly	Pro	Ile	Ile	Met	Ile	145	150	155
Ser	Tyr	Ala	Asp	Glu	Asn	Glu	Ala	Lys	Val	Ile	Thr	Trp	Lys	Asn	Ile	165	170	175
Asp	Leu	Pro	Tyr	Val	Glu	Val	Val	Ser	Ser	Glu	Arg	Glu	Met	Ile	Lys	180	185	190
Arg	Phe	Leu	Arg	Ile	Ile	Arg	Glu	Lys	Asp	Pro	Asp	Ile	Ile	Val	Thr	195	200	205
Tyr	Asn	Gly	Asp	Ser	Phe	Asp	Phe	Pro	Tyr	Leu	Ala	Lys	Arg	Ala	Glu	210	215	220
Lys	Leu	Gly	Ile	Lys	Leu	Thr	Ile	Gly	Arg	Asp	Gly	Ser	Glu	Pro	Lys	225	230	235
Met	Gln	Arg	Ile	Gly	Asp	Met	Thr	Ala	Val	Glu	Val	Lys	Gly	Arg	Ile	245	250	255
His	Phe	Asp	Leu	Tyr	His	Val	Ile	Thr	Arg	Thr	Ile	Asn	Leu	Pro	Thr	260	265	270
Tyr	Thr	Leu	Glu	Ala	Val	Tyr	Glu	Ala	Ile	Phe	Gly	Lys	Pro	Lys	Glu	275	280	285
Lys	Val	Tyr	Ala	Asp	Glu	Ile	Ala	Lys	Ala	Trp	Glu	Ser	Gly	Glu	Asn	290	295	300
Leu	Glu	Arg	Val	Ala	Lys	Tyr	Ser	Met	Glu	Asp	Ala	Lys	Ala	Thr	Tyr	305	310	315
Glu	Leu	Gly	Lys	Glu	Phe	Leu	Pro	Met	Glu	Ile	Gln	Leu	Ser	Arg	Leu	325	330	335
Val	Gly	Gln	Pro	Leu	Trp	Asp	Val	Ser	Arg	Ser	Ser	Thr	Gly	Asn	Leu	340	345	350
Val	Glu	Trp	Phe	Leu	Leu	Arg	Lys	Ala	Tyr	Glu	Arg	Asn	Glu	Val	Ala	355	360	365
Pro	Asn	Lys	Pro	Ser	Glu	Glu	Glu	Tyr	Gln	Arg	Arg	Leu	Arg	Glu	Ser	370	375	380
Tyr	Thr	Gly	Gly	Phe	Val	Lys	Glu	Pro	Glu	Lys	Gly	Leu	Trp	Glu	Asn	385	390	395
Ile	Val	Tyr	Leu	Asp	Phe	Arg	Ala	Leu	Tyr	Pro	Ser	Ile	Ile	Ile	Thr	405	410	415
His	Asn	Val	Ser	Pro	Asp	Thr	Leu	Asn	Leu	Glu	Gly	Cys	Lys	Asn	Tyr	420	425	430
Asp	Ile	Ala	Pro	Gln	Val	Gly	His	Lys	Phe	Cys	Lys	Asp	Ile	Pro	Gly	435	440	445
Phe	Ile	Pro	Ser	Leu	Leu	Gly	His	Leu	Leu	Glu	Glu	Arg	Gln	Lys	Ile	450	455	460
Lys	Thr	Lys	Met	Lys	Glu	Thr	Gln	Asp	Pro	Ile	Glu	Lys	Ile	Leu	Leu	465	470	475
Asp	Tyr	Arg	Gln	Lys	Ala	Ile	Lys	Leu	Leu	Ala	Asn	Ser	Phe	Tyr	Gly	485	490	495
Tyr	Tyr	Gly	Tyr	Ala	Lys	Ala	Arg	Trp	Tyr	Cys	Lys	Glu	Cys	Ala	Glu	500	505	510
Ser	Val	Thr	Ala	Trp	Gly	Arg	Lys	Tyr	Ile	Glu	Leu	Val	Trp	Lys	Glu	515	520	525
Leu	Glu	Glu	Lys	Phe	Gly	Phe	Lys	Val	Leu	Tyr	Ile	Asp	Thr	Asp	Gly	530	535	540
Leu	Tyr	Ala	Thr	Ile	Pro	Gly	Gly	Glu	Ser	Glu	Glu	Ile	Lys	Lys	Lys	545	550	555
Ala	Leu	Glu	Phe	Val	Lys	Tyr	Ile	Asn	Ser	Lys	Leu	Pro	Gly	Leu	Leu	565	570	575
Glu	Leu	Glu	Tyr	Glu	Gly	Phe	Tyr	Lys	Arg	Gly	Phe	Phe	Val	Thr	Lys	580	585	590
Lys	Arg	Tyr	Ala	Val	Ile	Asp	Glu	Gly	Lys	Val	Ile	Thr	Arg	Gly		595	600	605

Leu	Glu	Ile	Val	Arg	Arg	Asp	Trp	Ser	Glu	Ile	Ala	Lys	Glu	Thr	Gln
610						615					620				
Ala	Arg	Val	Leu	Glu	Thr	Ile	Leu	Lys	His	Gly	Asp	Val	Glu	Glu	Ala
625					630					635					640
Val	Arg	Ile	Val	Lys	Glu	Val	Ile	Gln	Lys	Leu	Ala	Asn	Tyr	Glu	Ile
				645					650					655	
Pro	Pro	Glu	Lys	Leu	Ala	Ile	Tyr	Glu	Gln	Ile	Thr	Arg	Pro	Leu	His
			660					665					670		
Glu	Tyr	Lys	Ala	Ile	Gly	Pro	His	Val	Ala	Val	Ala	Lys	Lys	Leu	Ala
		675						680				685			
Ala	Lys	Gly	Val	Lys	Ile	Lys	Pro	Gly	Met	Val	Ile	Gly	Tyr	Ile	Val
	690					695					700				
Leu	Arg	Gly	Asp	Gly	Pro	Ile	Ser	Asn	Arg	Ala	Ile	Leu	Ala	Glu	Glu
705					710					715					720
Tyr	Asp	Pro	Lys	Lys	His	Lys	Tyr	Asp	Ala	Glu	Tyr	Tyr	Ile	Glu	Asn
			725						730					735	
Gln	Val	Leu	Pro	Ala	Val	Leu	Arg	Ile	Leu	Glu	Gly	Phe	Gly	Tyr	Arg
		740						745					750		
Lys	Glu	Asp	Leu	Arg	Tyr	Gln	Lys	Thr	Arg	Gln	Val	Gly	Leu	Thr	Ser
		755						760				765			
Trp	Leu	Asn	Ile	Lys	Lys	Ser	Gly	Thr	Gly	Gly	Gly	Gly	Ala	Thr	Val
	770					775						780			
Lys	Phe	Lys	Tyr	Lys	Gly	Glu	Glu	Lys	Glu	Val	Asp	Ile	Ser	Lys	Ile
785					790					795					800
Lys	Lys	Val	Trp	Arg	Val	Gly	Lys	Met	Ile	Ser	Phe	Thr	Tyr	Asp	Glu
			805						810					815	
Gly	Gly	Gly	Lys	Thr	Gly	Arg	Gly	Ala	Val	Ser	Glu	Lys	Asp	Ala	Pro
			820					825					830		
Lys	Glu	Leu	Gln	Met	Leu	Glu	Lys	Gln	Lys	Lys					
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<210> 9  
 <211> 1904  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: fusion protein  
 Sac7d-deltaTaq

<220>  
 <221> CDS  
 <222> (1)..(1904)  
 <223> Sac7d-deltaTaq

<400> 9  
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 gacaatggta agacaggtag aggagctgta agcgagaaag atgctccaaa agaattatta 180  
 gacatgttag caagagcaga aagagagaag aaaggcggcg gtgtcactag tccaagggcc 240  
 ctggaggagg ccccttgagg cccgcgggaa ggggccttcg tgggctttgt gctttcccg 300  
 aaggagccca tgtgggcccga tcttctggcc ctggccgccg ccaggggggg ccgggtccac 360  
 cgggcccccg agccttataa agccctcagg gacctgaagg aggcgcgggg gcttctcgcc 420  
 aaagacctga cgttctggc cctgagggaa ggccttgccc tccgcggcg cgacgacccc 480  
 atgctcctcg cctacctcct ggacccttcc aacaccaccc ccgagggggg ggcccggcgc 540  
 tacggcgggg agtgagcggg ggagggcggg gagcgggccg ccctttccga gaggctcttc 600  
 gccaacctgt gggggaggct tgagggggag gagaggctcc tttggcttta ccgggagggtg 660  
 gagaggcccc tttccgctgt cctggccccc atggaggcca cgggggtgcg cctggacgtg 720  
 gcctatctca gggccttgct cctggagggt gccgaggaga tcgcccgcct cgaggccggg 780  
 tcttccgcct ggccggccac cccttcaacc tcaactcccg ggaccagctg gaaagggtcc 840

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tctttgacga gctagggcctt cccgccatcg gcaagacgga gaagaccggc aagcgctcca 900
ccagcgccgc cgtcctggag gccctccgcg agggccaccc catcgtggag aagatcctgc 960
agtaccggga gctcaccaag ctgaagagca cctacattga ccccttgccg gacctcatcc 1020
accccaggac gggccgcctc cacaccgct tcaaccagac ggccacggcc acgggcaggc 1080
taagtagctc cgatcccaac ctccagaaca tccccgtccg caccctcgctt gggcagagga 1140
tccgccgggc cttcatcgcc gaggaggggt ggctattggt ggccctggac tatagccaga 1200
tagagctcag ggtgctggcc cacctctccg gcgacgagaa cctgatccgg gtcttccagg 1260
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agggcaccgc cgccgacctc atgaagctgg ctatggtgaa gctcttcccc aggctggagg 1680
aaatgggggc caggatgctc cttcaggtcc acgacgagct ggtcctcgag gccccaaaag 1740
agagggcgga ggccgtggcc cggctggcca aggaggtcat ggaggggggtg tatcccctgg 1800
ccgtgcccct ggaggtggag gtggggatag gggaggactg gctctccgcc aaggagggca 1860
ttgatggccg cggcggaggc gggcatcatc atcatcatca ttaa 1904

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<210> 10

<211> 634

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: fusion protein  
Sac7d-deltaTaq

<400> 10

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Glu Lys Glu Val Asp Thr Ser Lys Ile Lys Lys Val Trp Arg Val Gly
             20             25             30
Lys Met Val Ser Phe Thr Tyr Asp Asn Gly Lys Thr Gly Arg Gly
             35             40             45
Ala Val Ser Glu Lys Asp Ala Pro Lys Glu Leu Leu Asp Met Leu Ala
             50             55             60
Arg Ala Glu Arg Glu Lys Lys Gly Gly Gly Val Thr Ser Pro Lys Ala
             65             70             75             80
Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe
             85             90             95
Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp Leu Leu Ala Leu Ala
             100            105            110
Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala
             115            120            125
Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser
             130            135            140
Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro
             145            150            155            160
Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly
             165            170            175
Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg
             180            185            190
Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu Glu
             195            200            205
Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu
             210            215            220
Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val
             225            230            235            240

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<220>  
 <221> CDS  
 <222> (1) .. (1965)  
 <223> PL-deltaTaq

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<400> 11
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gaggtagaca tctccaagat caagaaagta tggcgtgtgg gcaagatgat ctcccttcacc 180
tacgacgagg gcggtggcaa gaccggccgt ggtgcggtaa gcgaaaagga cgcgccgaag 240
gagctgctgc agatgctgga gaagcagaaa aaggcgggcg gtgtcaccag tcccaaggcc 300
ctggaggagg cccctggcc cccgccgga ggggccttcg tgggctttgt gctttcccg 360
aaggagccca tgtgggcccga tcttctggcc ctggccgccg ccagggggggg ccgggtccac 420
cgggcccccg agccttataa agccctcagg gacctgaagg aggcgcgggg gcttctcgcc 480
aaagacctga gcgttctggc cctgagggaa ggccttggcc tcccgcccg cgacgacccc 540
atgctcctcg cctacctcct ggaccttcc aacaccaccc ccgagggggg ggcccggcgc 600
tacggcgggg agtggacgga ggaggcgggg gagcggggcg ccctttccga gaggctcttc 660
gccaaacctgt gggggaggct tgagggggag gagaggctcc tttggcttta ccgggaggtg 720
gagaggcccc tttccgctgt cctggcccac atggaggcca cgggggtgcg cctggacgtg 780
gcctatctca gggccttgtc cctggaggtg gccgaggaga tcgcccgcct cgaggccgag 840
gtcttccgcc tggccggcca ccccttcaac ctcaactccc gggaccagct ggaaagggtc 900
ctctttgacg agctagggtt tcccgccatc ggcaagacgg agaagaccgg caagcgctcc 960
accagcgccg ccgtcctgga ggccctccgc gaggccacc ccatcggtga gaagatcctg 1020
cagtaccggg agctcaccaa gctgaagagc acctacattg accccttgcc ggacctcatc 1080
caccccagga cgggccgcct ccacaccgc ttcaaccaga cggccacggc cacgggcagg 1140
ctaagtagct ccgatcccaa cctccagaac atccccgtcc gcaccccgct tgggcagagg 1200
atccgcgggg ccttcacgct cgaggagggg tggctattgg tggccctgga ctatagccag 1260
atagagctca ggggtgctggc ccacctctcc ggcgacgaga acctgatccg ggtcttccag 1320
gaggggcggg acatccacac ggagaccgcc agctggatgt tcggcgctcc ccgggaggcc 1380
gtggaccccc tgatgcgccg ggcgcccaag accatcaact tcggggctct ctacggcatg 1440
tcggccacc gcctctccca ggagctagcc atcccttacg aggaggcca ggccttcatt 1500
gagcgctact ttcagagctt cccaagggtg cgggcctgga ttgagaagac cctggaggag 1560
ggcaggaggc gggggtacgt ggagaccctc ttcggccgcc gccgctacgt gccagacct 1620
gaggcccggt tgaagagcgt gcgggaggcg gccgagcgca tggccttcaa catgccgctc 1680
cagggcaccg ccgccgacct catgaagctg gctatggtga agctcttccc caggctggag 1740
gaaatggggg ccaggatgct ccttcagggt cagcagcagc tggctctcga ggcccaaaa 1800
gagagggcgg aggcctgggc ccggctggcc aaggaggtca tggagggggg gtatccctg 1860
gccgtgcccc tggaggtgga ggtggggata ggggaggact ggctctccgc caaggagggc 1920
attgatggcc gcggcgaggg cgggcatcat catcatcatc attaa 1965
```

<210> 12  
 <211> 654  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:fusion protein  
 PL-deltaTaq

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<400> 12
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Lys Lys Lys Lys Lys Gly Gly Gly Val Thr Ser Gly Ala Thr Val Lys
20      25      30
Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile Lys
35      40      45
Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu Gly
50      55      60
Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro Lys
65      70      75      80
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Glu	Leu	Leu	Gln	Met	Leu	Glu	Lys	Gln	Lys	Lys	Gly	Gly	Gly	Val	Thr	85	90	95
Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	Ala	100	105	110
Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala	Asp	Leu	115	120	125
Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala	Pro	Glu	130	135	140
Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu	Leu	Ala	145	150	155
Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu	Pro	Pro	165	170	175
Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn	Thr	180	185	190
Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu	Glu	195	200	205
Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn	Leu	Trp	210	215	220
Gly	Arg	Leu	Glu	Gly	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg	Glu	Val		225	230	235
Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr	Gly	Val	245	250	255
Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	Ala	Glu	260	265	270
Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	His	Pro	275	280	285
Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp	Glu	290	295	300
Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	Arg	Ser	305	310	315
Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile	Val	325	330	335
Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	Thr	Tyr	340	345	350
Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	Leu	His	355	360	365
Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser	370	375	380
Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	Arg	385	390	395
Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	Ala	Leu	405	410	415
Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	Asp	420	425	430
Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr	Glu	435	440	445
Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	Pro	Leu	450	455	460
Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	465	470	475
Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu	Ala	485	490	495
Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg	Ala	500	505	510
Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	Val	Glu	515	520	525
Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	Arg	Val	530	535	540
Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	Val	545	550	555

Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe  
                                   565                                  570                                  575  
 Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His Asp  
                                   580                                  585                                  590  
 Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg  
                                   595                                  600                                  605  
 Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu  
                                   610                                  615                                  620  
 Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu Gly  
 625                                  630                                  635                                  640  
 Ile Asp Gly Arg Gly Gly Gly Gly His His His His His His  
                                   645                                  650

<210> 13  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer L71F

<400> 13  
 cctgctctgc cgcttcacgc 20

<210> 14  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer L71R

<400> 14  
 gcacagcggc tggctgagga 20

<210> 15  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer L18015F

<400> 15  
 tgacggagga taacgccagc ag 22

<210> 16  
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<210> 20  
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<210> 21  
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<210> 22  
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<210> 23  
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<400> 23  
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<210> 24  
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<210> 25  
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<400> 25  
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<210> 26  
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<210> 27  
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<210> 28  
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beta-globin primer Bglbn536R

<400> 28  
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<210> 29  
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beta-globin primer Bglbn1408R

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<210> 30  
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tag

<400> 30  
His His His His His His  
1 5

<210> 31  
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<212> PRT  
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<220>  
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epitope tag

<400> 31  
Asp Tyr Lys Asp Asp Asp Asp Lys  
1 5

<210> 32  
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<212> PRT  
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<220>  
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<400> 32  
Gly Gly Val Thr  
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<210> 33  
<211> 6  
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<220>  
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<400> 33  
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<210> 34  
<211> 21  
<212> PRT  
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peptide

<400> 34  
Asn Ser Lys Lys Lys Lys Lys Lys Lys Arg Lys Lys Arg Lys Lys Lys  
1 5 10 15  
Gly Gly Gly Val Thr  
20